

FIG. 1 Alignment of mouse sequences with the human chromosome 12 genomic clone NT_009720

Expect = 4e-28, Identities = 179/224 (79%), Gaps = 4/224 (1%)

Query: 696 ctttgggacagtgaagctgcctttcatagaaaaatggccttgtgctcctgcttcagcca 755
||||| ||||||||| ||||||||| |||| | ||||||||| | ||||
Sbjct: 315187 ctttgggtgcagtgaagagccgcctttcataggaaaacagt-ttgtgctcctgactgggcca 315129

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Query: 756 cctttcacccctgctcgatt-gcggagcatgtggtgagagg-cagggataaaagggctca 813
||||| |||| | | | | | ||| |||| | |||| ||||
sbjct: 315128 cctttcaccccttgttcaagtacgagctcatttgtaaggggtcaggaataaaagggctct 315069

Query: 814 ctctgccctttccatgtgcaggaagtggccccaggagtgaggagtggtgtgtcccaaat 873
||| |||| ||||||| ||||||| |||| ||||||| ||| |||||||
Sbjct: 315068 ttcttcctctccatgtgtaggaagtccagcccttggtgtggagagtcatttctcaaat 315009

Query: 874 aga-cttcctaatacacagttcccaagaaggccaagagtcagtca 916
||| ||||||||| ||||||||| ||||||||| |||||||||
Sbjct: 315008 agatcttcctaatatggttcccaagaaggccaagagtcagtca 314965

FIG. 2 The Human RFX4 Locus

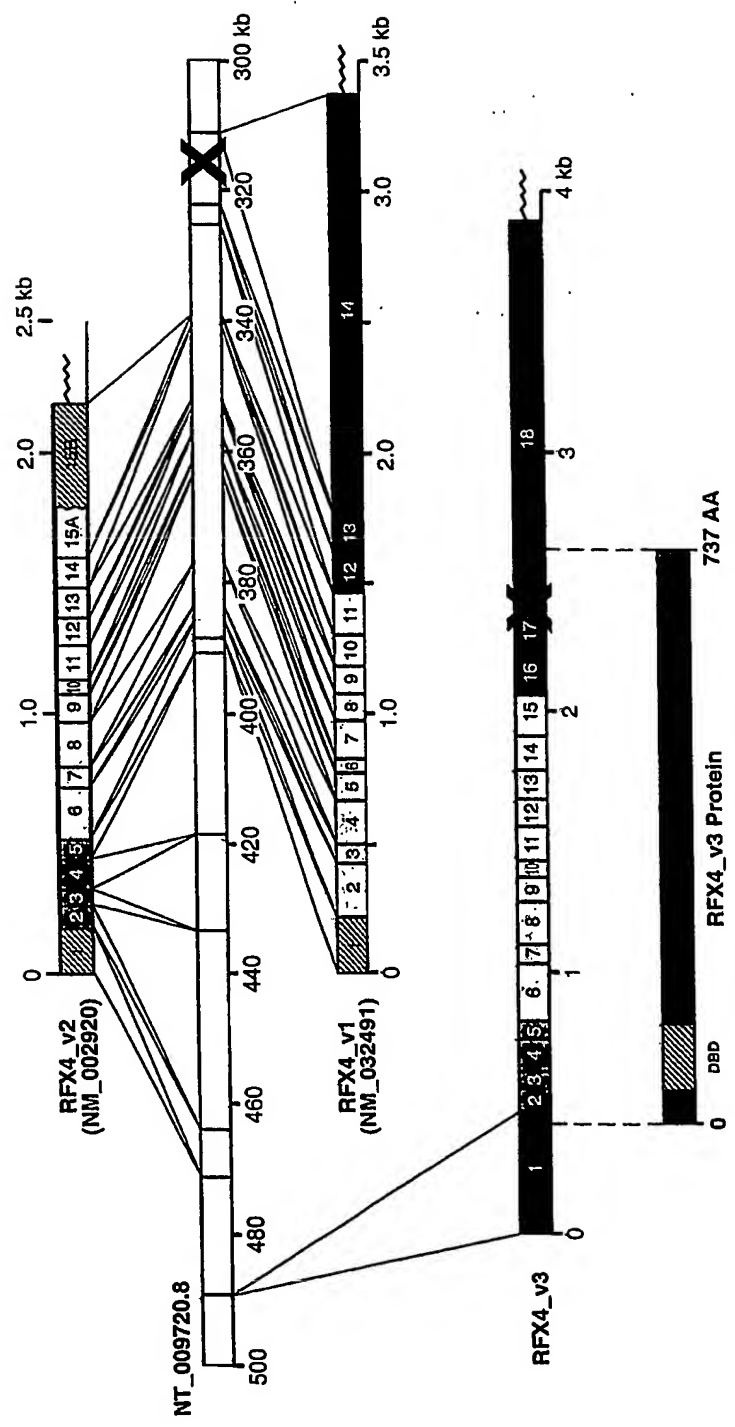


FIG. 3 Alignment of human and mouse proximal promoters for RFX4_v3

Expect = e-107

Identities = 212/216 (98%)

Human 786 gaggggcccacatctaagcccaatttttgatttcgcctataatgagtgccggcggaaggctg 845
||||| || ||||||||||||||||||| ||||||||||||||| |||||||
Mouse 86 gagggggcagatctaagcccaatttttgatttcgctctataatgagtgccggcggaaggctg 145

Human 846 gagaaggcctctggaaactttaataaagaaaaacgttgctaataataagaagggga 905
||||| ||||||||||||||||||| ||||||||||||||| |||||||
Mouse 146 gagaaggcctctggaaactttaataaagaaaaacgttgctaataataagaagggga 205

Human 906 agtcggagggctgggattgcgtcgctctgagcccccccttttcggaggcggttttcttat 965
||||| ||||||||||||||||||| ||||||||||||||| |||||||
Mouse 206 agtcggagggctgggattgcgtcgctctgagcccccccttttcggaggcggttttcttat 265

Human 966 tcaaaaacaggccccacaaatgggcttcac 992
||||| ||||||||||||||||||| |||||||
Mouse 266 tcaaaaacaggccccacaaatgggcttcac 292

FIG. 4 Human, mouse, and zebrafish alignment of RFX4_v3 (amino terminus)

[illegible]

FIG. 5 Alignment of human and mouse RFX4_v3

human	MHCGLEEPDMDSTESWIEPCLNESENKPYSSHTSLGNVSDNENEKENNRASKPHSTPATLQWLEENYEIAEGVCIPRSALYMHYLDCEKNDTQPVNAASFGKIIROQFPQLTTRPLG 120
mouse	MHCGLEEPDMDSTESWIEPCLNESENKPYSSHTSLGNVSDNENEKENNRASKPHSTPATLQWLEENYEIAEGVCIPRSALYMHYLDCEKNDTQPVNAASFGKIIROQFPQLTTRPLG 120
human	T--RGQSKYHYGIAVRESSQYVDVMSKGAAMVSETGKAEVSKOTVAYSPPSKLGLTLLPEFPNVKDLNLPASLPEEKVSTFIMMYRTHCQILLDTVIRANEDEVQSEFLHFWQGMPPH 238
mouse	TGTFGQSKYHYGIAVRESSQYVDVMSKGAAMVSETGKAEVSKOTVAYSPPSKLGLTLLPEFPNVKDLNLPASLPEEKVSTFIMMYRTHCQILLDTVIRANEDEVQSEFLHFWQGMPPH 240
human	MLPVLGSSTVNVIGVCDISILYAISGVLMPTVLQALPDSLTQVIRKFAKQDDEWLAVALHDLPENLENIFELSRFSQILRRQTSLNHLCOASFTVIHSADITFQMLEDMKNVDLNSI 358
mouse	MLPVLGSSTVNVIGVCDISILYAISGVLMPTVLQALPDSLTQVIRKFAKQDDEWLAVALHDLPENLENIFELSRFSQILRRQTSLNHLCOASFTVIHSADITFQMLEDMKNVDLSSI 360
human	TKQTLTYMEDSDNDEHKLLITQLYQEFDFHLLLEEQSPIESYIEWLDTMVDKCVVVAARKQGSLKVAQQFLMWSQFGRVIFDMTLHSAPSGFSEHLLHLMEDDYVLYLLESLLHCOEPAN 478
mouse	TKQTLTYMEDSDNDEHKLLITQLYQEFDFHLLLEEQSPIESYIEWLDTMVDKCVVVAARKQGSLKVAQQFLMWSQFGRVIFDMTLHSAPSGFSEHLLHLMEDDYVLYLLESLLHCOEPAN 480
human	ELMRAMKGEGSTAEVNEEIIILTEAAAPTSPVPSPSPAKSATSVEVPPSPSPVSNPSPPEYTGISTGAMQSYTWSLTYYTTAAGSPAENSQQLPCMRNTHVPSSSVTHPIPVYPHKEEH 598
mouse	ELMRAMKGEGSTAEVNEEIIILTEATEPTSPGSPSPAKSATSVEVPPSPSPVSNPSPPEYTGISTGAMQSYTWSLTYYTTAAGSPAENSQQLPCMRNTHVPSSSVTHKIPVYSHHEEH 600
human	GYTGSYNYGSYGNQHPPHMQSQYPALPHDTAISGPLHYAPYHSSAQYFENSPTSNEPCLMSSTPPLHPTFVTPRWPEVPTANACTSPSVHSTFYGNSSDMYTPLTTRNSEYEHMQH 718
mouse	GYTGSYNYGSYGNQHPPHMQSQYPALPHDTAISGPLHYSPYHRSSAQYFENSPTSMEPCLMSSTPPLHPTFVTPRWPEVPTANACTSPSVHSTFYGNSSDMYTPLTTRNSEYEHMQH 720
human	FPGFAYINGEASTGWAK 735
mouse	FPGFAYINGEASTGWAK 737

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Exon 1

Human MHCGLLEPDMSTESWIERCLNESENKRYSSHTSLGNVNDENEKENNRASKPHSTPA 60
 Mouse MHCGLLEPDMSTESWIERCLNESENKRYSSHTSLGNVNDENEKENNRASKPHSTPA 60
 Zebrafish MLCGLLEPDMSTESWIERCLNESESKRFSSHSSIGNISNDENEKENNRASKPHSTPA 60
 * * * * *

Exons 2-5

TLQWLEENYEIAEGVCIPRSALYMHYLDCEKNDTPVNAASFGKIIROQFPOLTRRLG 120
 TLQWLEENYEIAEGVCIPRSALYMHYLDCEKNDTPVNAASFGKIIROQFPOLTRRLG 120
 TLQWLEENYEIAEGVCIPRIALYMHYLDCEKLDSPVNAASFGKIIROQFPOLTRRLG 120
 * * * * *

DBD

T--RGQSKYHYIYGIKVESSQYIDVMYSKKGAAWVSETGKKEVSKQTVAYSPPRSKLGTL 178
 TGTRGQSKYHYIYGIKVESSQYIDVMYSKKGAAWVSETGKREVTQTVAYSPPRSKLGTL 180
 T--RGQSKYHYIYGIKVESSQYIDVMYSKKGAAWVNETGKKEVTQTVAYSPPRSKLGTL 178
 * * * * *

PEFPNVKDINLPASLPEEKVSTFIMMYRTHCQRLDVTIRANFDEVQSFLIHFWGCMPPH 238
 PDEFNVKDINLPASLPEEKVSTFIMMYRTHCQRLDVTIRANFDEVQSFLIHFWGCMPPH 240
 PDEFNVKDINLPASLPEEKVSTFIMMYRTHCQRLDVTIRANFDEVQSFLIHFWGCMPPH 238
 * * * * *

B

MLPVLCSSSTVNVIVGVCDSTLYKATSGVLMPTVLOALEDSLTOVIRKFAKQDDEWLKVAL 298
 MLPVLCSSSTVNVIVGVCDSTLYKATSGVLMPTVLOALEDSLTOVIRKFAKQDDEWLKVAL 300
 MLPVLCSSSTVNVIVGVCDSTLYKATSGVLMPTVLOALEDSLTOVIRKFAKQDDEWLKVAL 298
 * * * * *

C

Exons 6-15

HDLPEENLNRIKFEISRFQSILRRQTSLNHLCOASRTVHSADITFQMLEDWNRVNLNSI 358
 HDLPEENLNRIKFEISRFQSILRRQTSLNHLCOASRTVHSADITFQMLEDWNRVNLSSI 360
 HDLPEENLNRIKFEISRFQSILRRQTSLNHLCOASRTVHSADITFQMLEDWNRVNLNSI 358
 * * * * *

TKQTLTYMEDSRDEHRRLTQLYQDFPHLLEEQSPIESYIEWLDMVDRCVVKAAKROG 418
 TKQTLTYMEDSRDEHRRLTQLYQDFPHLLEEQSPIESYIEWLDMVDRCVVKAAKROG 420
 TKQTLTYMEDSRDEHRRLTQLYQDFPHLLEEQSPIESYIEWLDMVDRCVVKAAKROG 418
 * * * * *

DD

SLKQVACQELLMSCECTRVIRDMTHSAPSGSGFHLIHLMFDDVLYLLESILHCOERAN 478
 SLKQVACQELLMSCECTRVIRDMTHSAPSGSGFHLIHLMFDDVLYLLESILHCOERAN 480
 SLKQVACQELLMSCECTRVIRDMTHSAPSGSGFHLIHLMFDDVLYLLESILHCOERAN 478
 * * * * *

EIMRAMKGECSAEVREETLLTEAAATPSPVPSFSPAKSATSMEVPPSPSPVNSPPEY 538
 EIMRAMKGECSAEVREETLLTEAAATPSPVPSFSPAKSATSMEVPPSPSPVNSPPEY 540
 EIMRAMKGECSAEVREETLLTEAAATPSPVPSFSPAKSATSMEVPPSPSPVNSPPEY 537
 * * * * *

TGLS--TGAMQSYTWSLTYYTVAAGSPAENSQQLPCMRN--THVPSSSVTHRIPVYPHRE 596
 TGLS--TGAMQSYTWSLTYYTVAAGSPAENSQQLPCMRN--THVPSSSVTHRIPVYPHRE 598
 TSISATTGAVQSYTWSLTYYTVAAGSPAENSQQLPCMRN--THVPSSSVTHRIPVYPHRE 597
 * * * * *

Exons 16-18

EHGYTGSYNYGSYGNQHPHMQSQYPALPHDTAISGPLHYAPYHRSSAQYPFNSPTSME 656
 EHGYTGSYNYGSYGNQHPHMQSQYPALPHDTAISGPLHYAPYHRSSAQYPFNSPTSME 658
 EHGYTGSYNYGSYGNQHPHMQSQYPALPHDTAISGPLHYAPYHRSSAQYPFNSPTSME 657
 * * * * *

PCLMSSTPRLHPTVPTPRWPEVPSANTCYTSPSVHSARYGNSSDMYPLTTRNSEYEHEM 716
 PCLMSSTPRLHPTVPTPRWPEVPSANTCYTSPSVHSARYGNSSDMYPLTTRNSEYEHEM 718
 SCLMSGSPILLHSPVTPRWPDPVPSANSCYSSPTVHASRYS--TGDMSYPLAPRRNSEYEHA 716
 * * * * *

QHFPGFAYINGEASTGWAK 735
 QHFPGFAYINGEASTGWAK 737
 QHFPGFAYINGEATTGWAK 735
 * * * * *

FIG. 6

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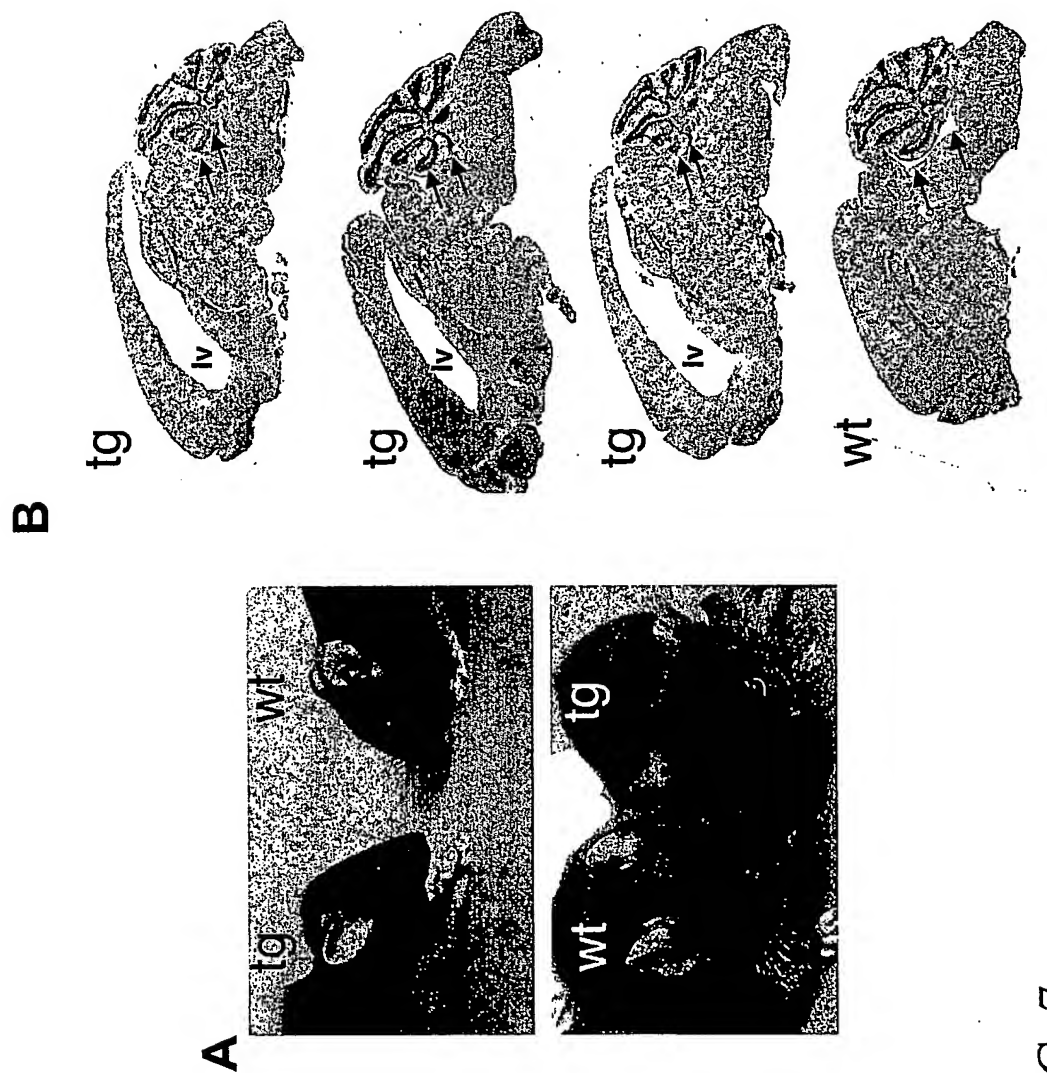


FIG. 7

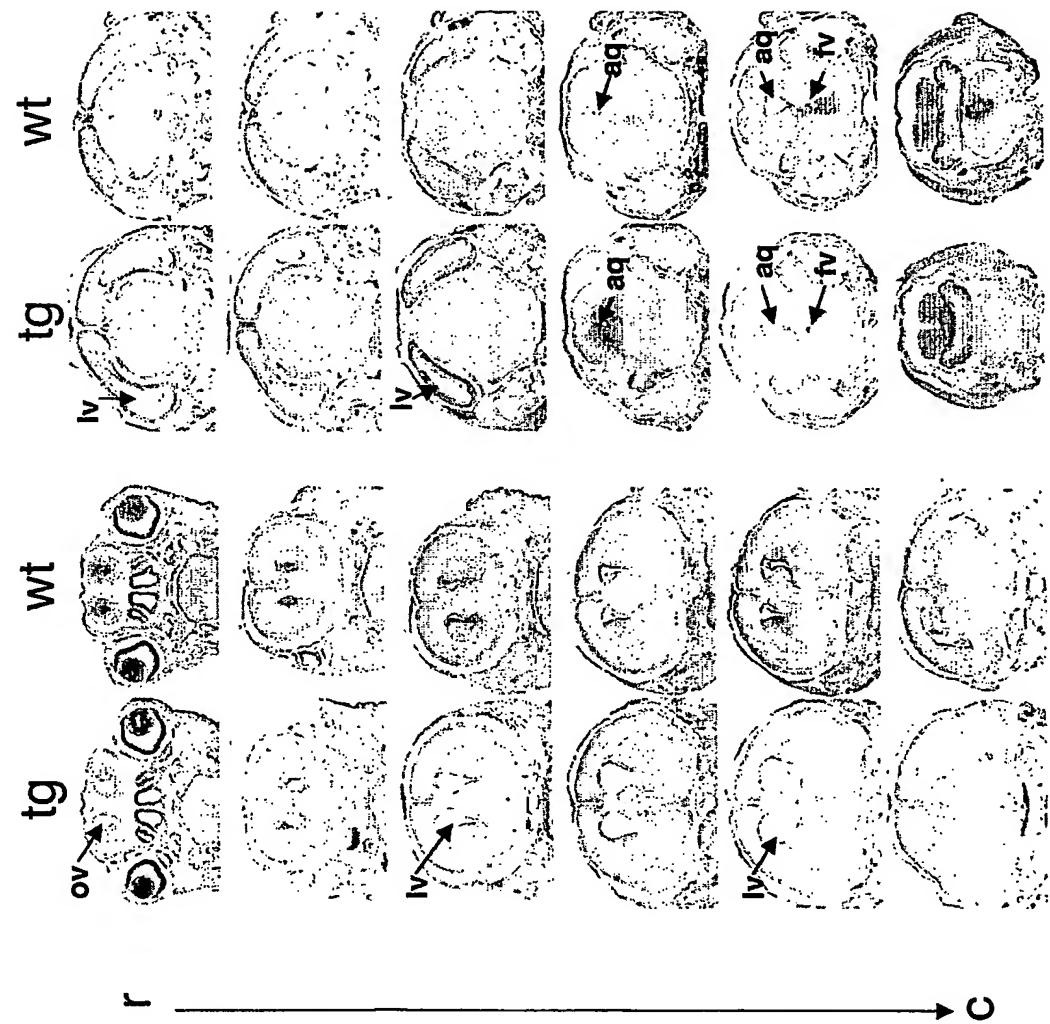


FIG. 8

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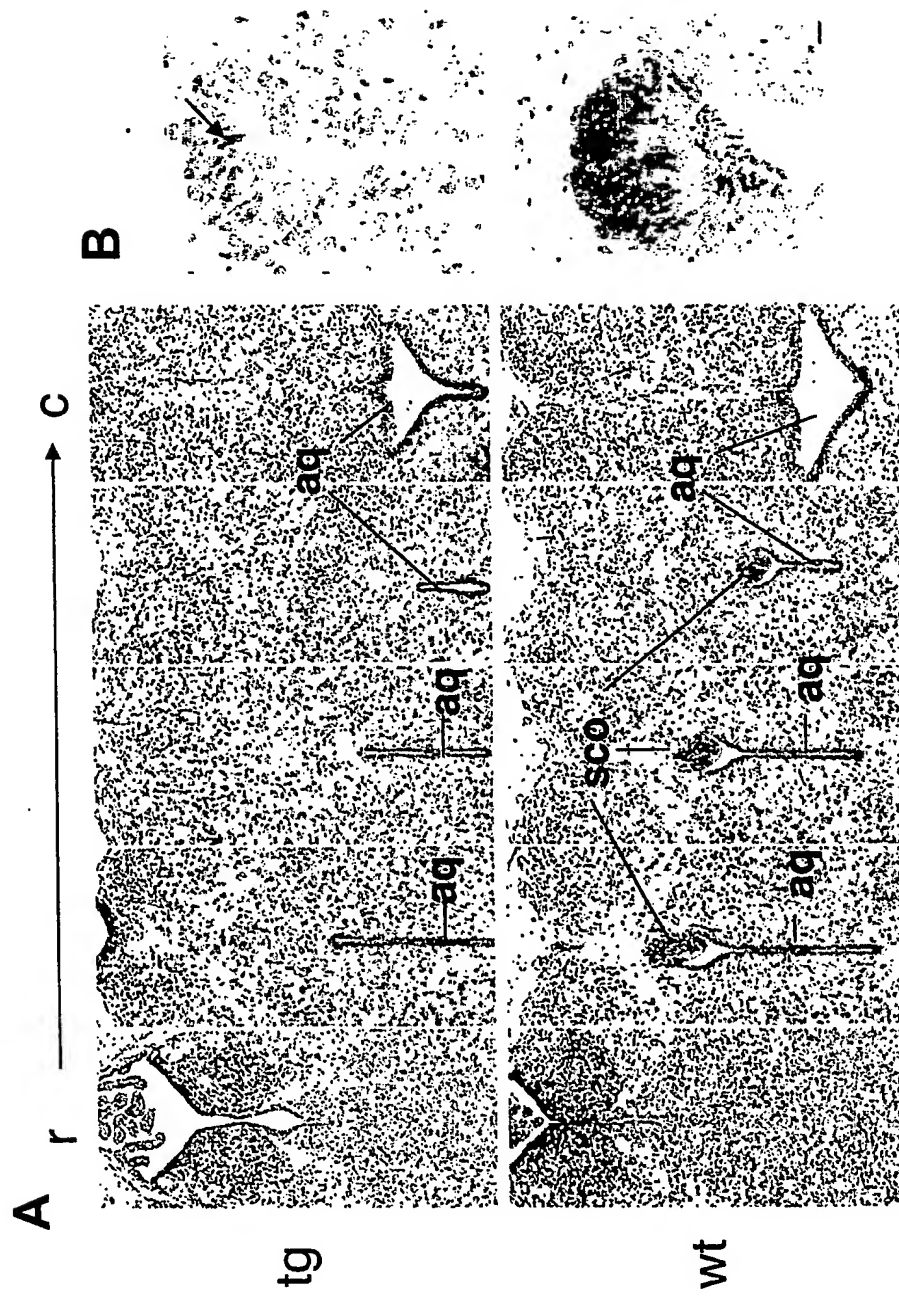


FIG. 9

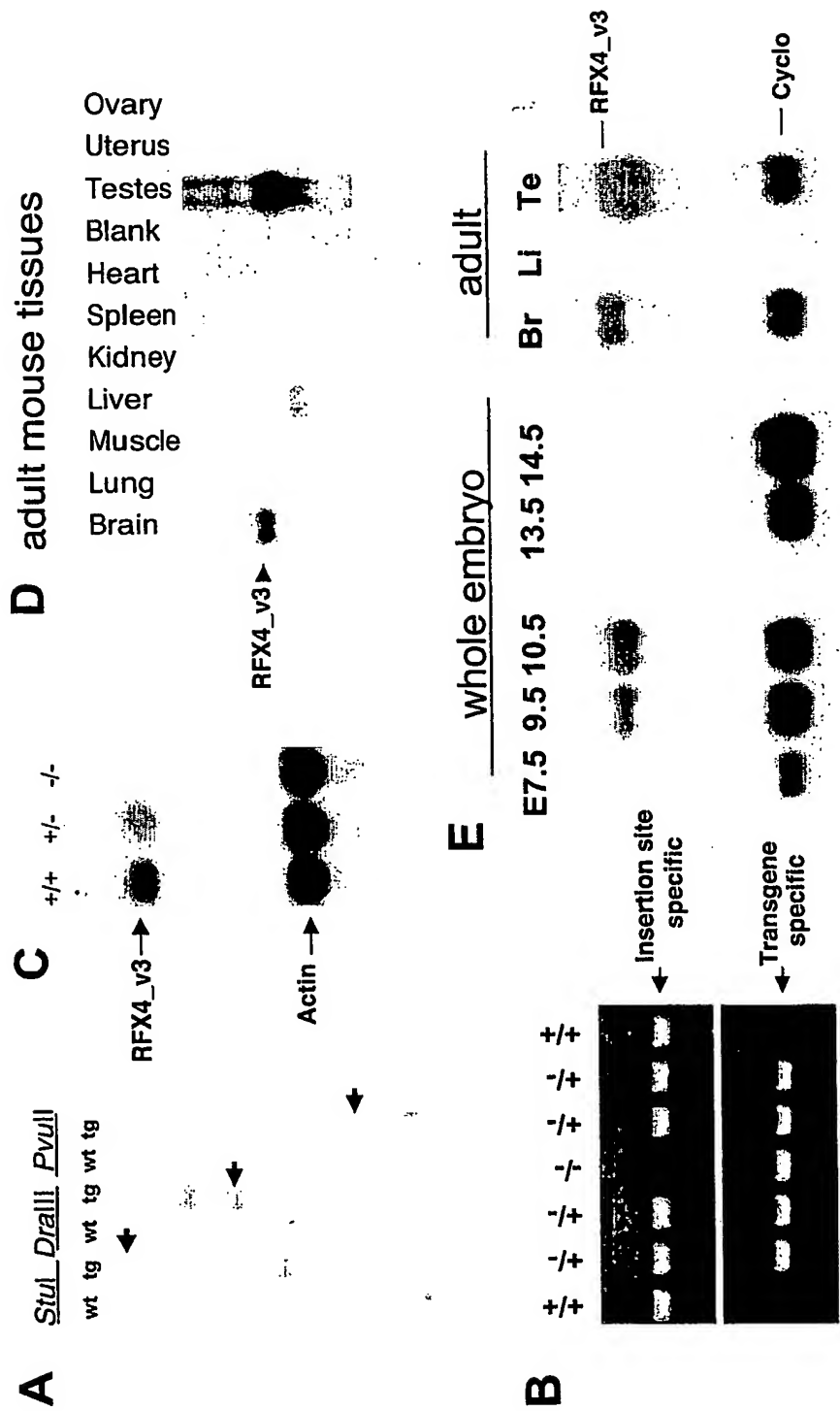


FIG. 10

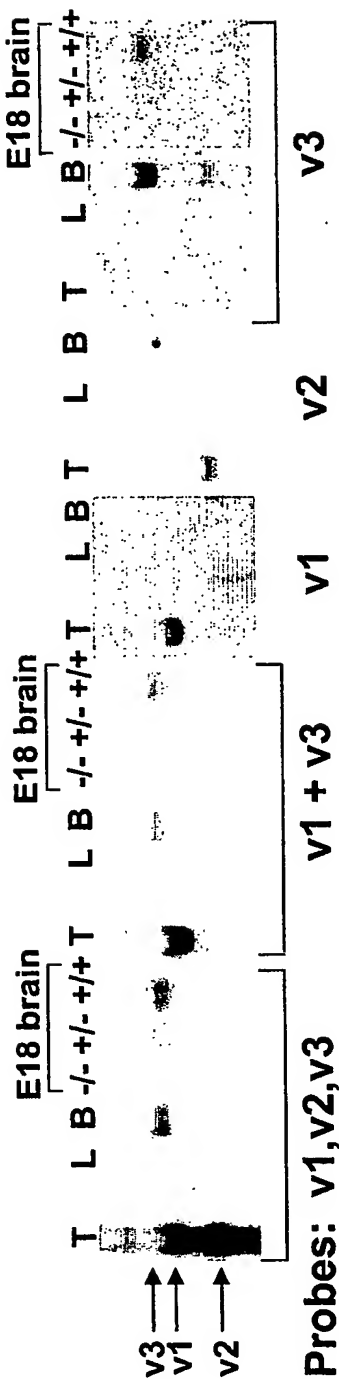


FIG. 11

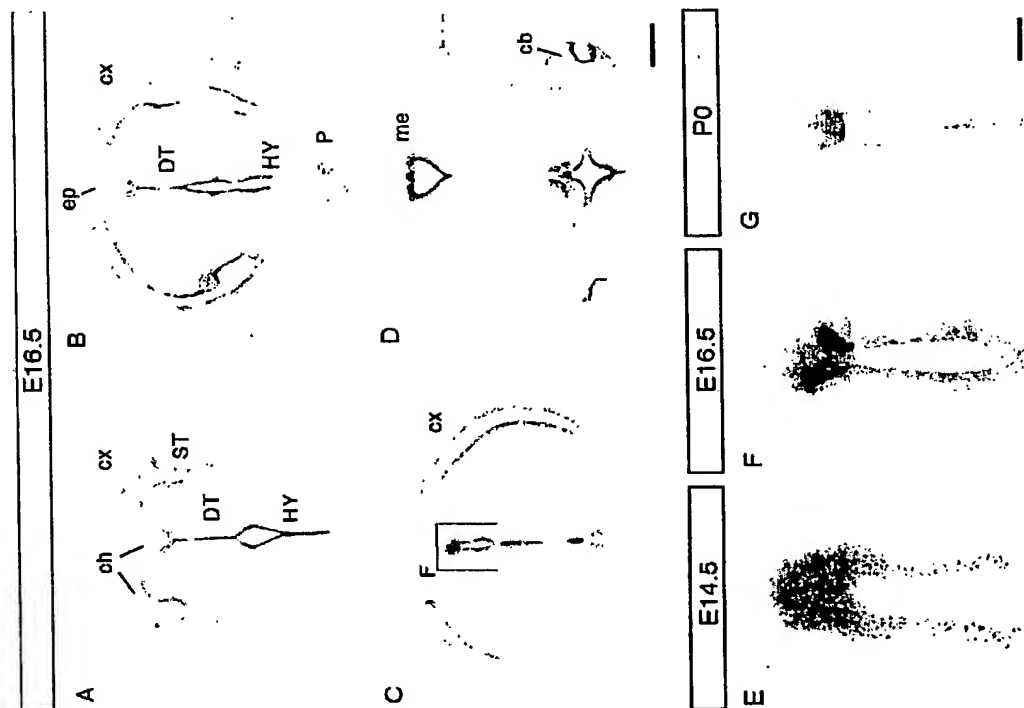


FIG. 13

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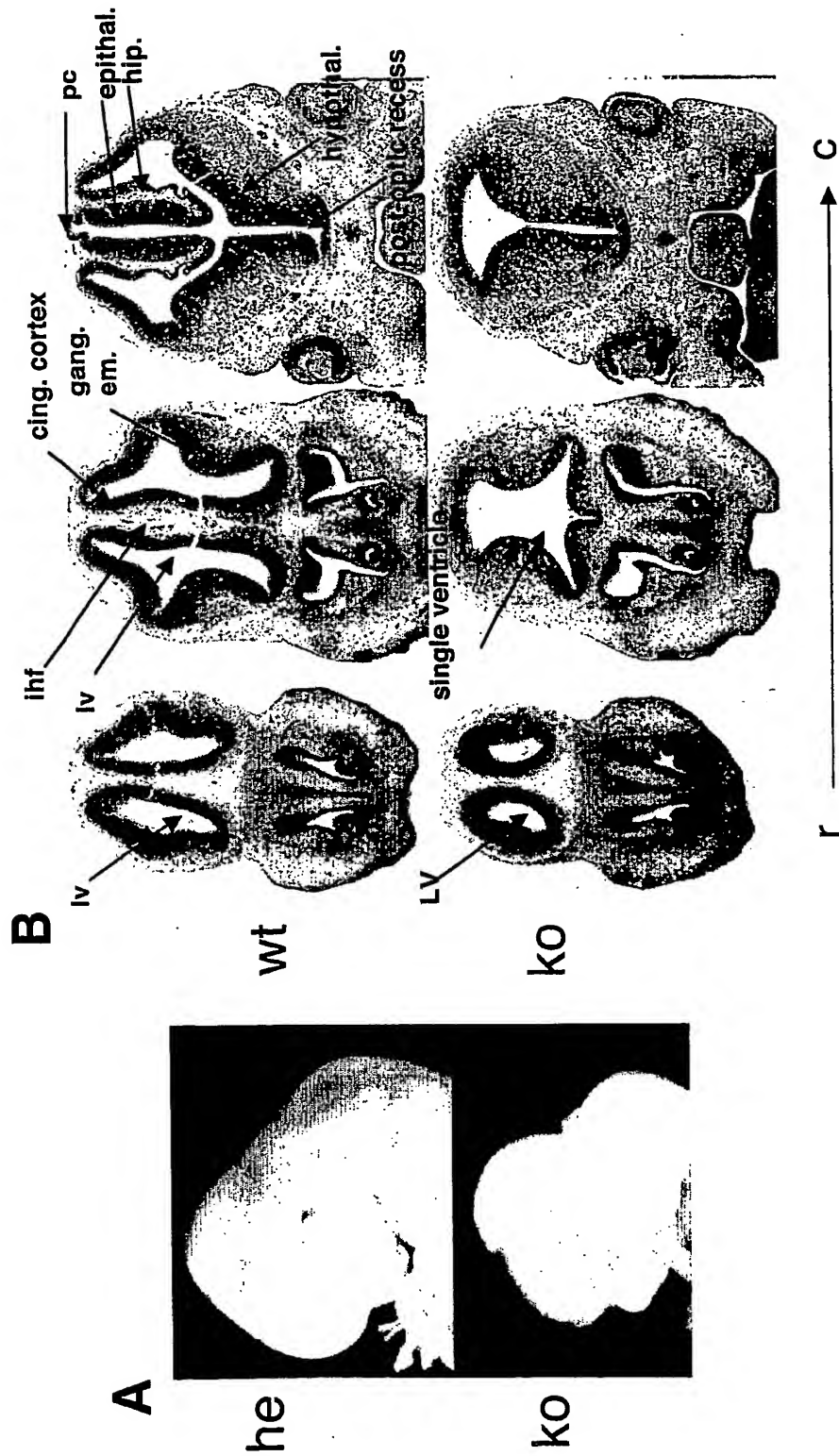


FIG. 14

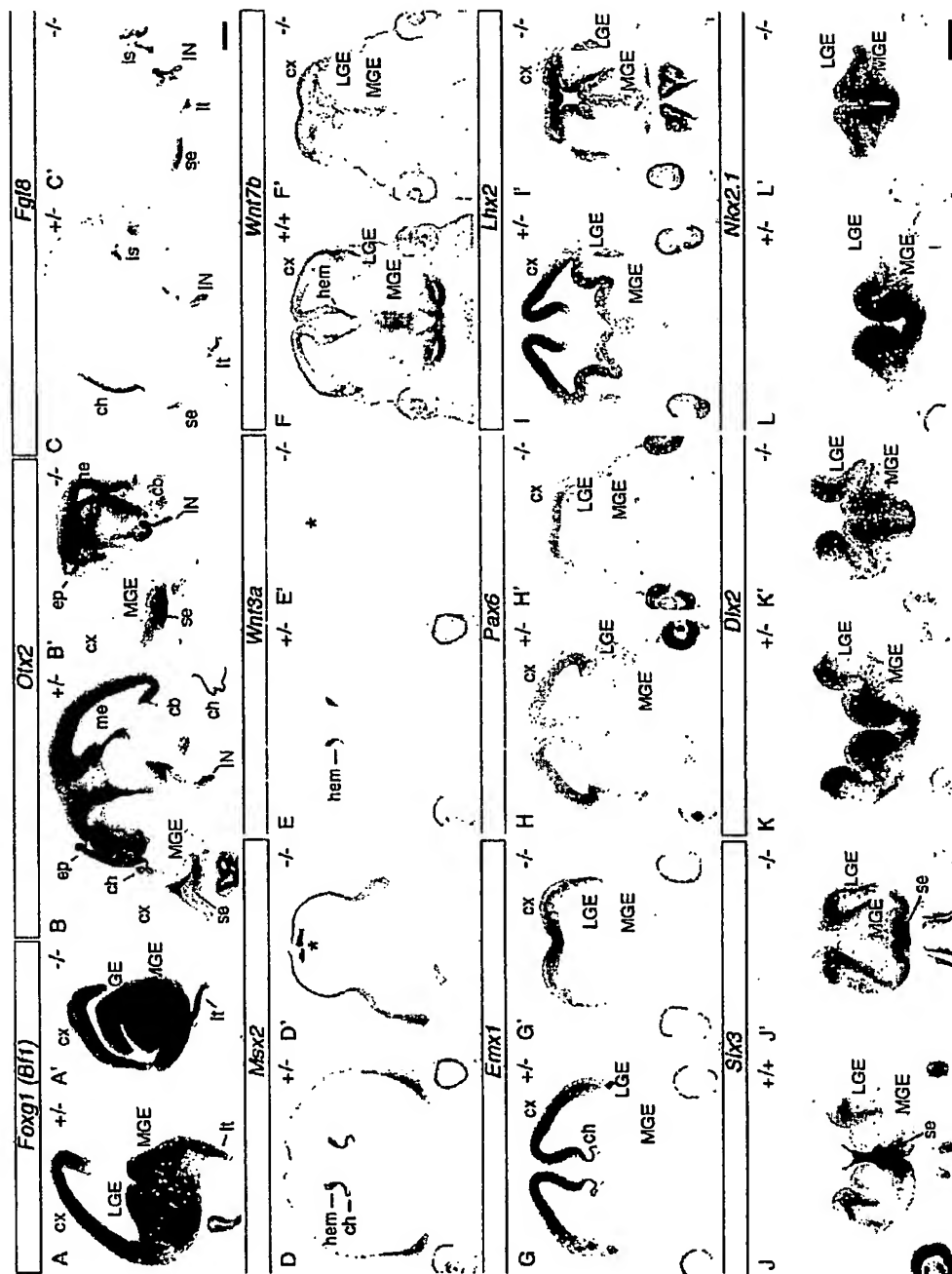


FIG. 15

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